



1600

#L

RAW SEQUENCE LISTING

DATE: 11/18/2002

PATENT APPLICATION: US/09/785,474A

TIME: 12:52:34

Input Set : A:\Sub_Seq_List_0609_4180002.txt

Output Set: N:\CRF4\11182002\I785474A.raw

5 <110> APPLICANT: Tanzi, Rudolph
 6 Wasco, Wilma
 9 <120> TITLE OF INVENTION: Genetic Alterations Related To Familial Alzheimer's Disease
 11 <130> FILE REFERENCE: 0609.4180002
 14 <140> CURRENT APPLICATION NUMBER: 09/785,474A
 15 <141> CURRENT FILING DATE: 2001-02-20
 18 <150> PRIOR APPLICATION NUMBER: US 08/706,344
 19 <151> PRIOR FILING DATE: 1996-08-30
 22 <150> PRIOR APPLICATION NUMBER: US 60/003,054
 23 <151> PRIOR FILING DATE: 1995-08-31
 26 <160> NUMBER OF SEQ ID NOS: 32
 29 <170> SOFTWARE: PatentIn version 3.1
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 2765
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Homo sapiens
 38 <220> FEATURE:
 39 <221> NAME/KEY: CDS
 40 <222> LOCATION: (249)..(1649)
 41 <223> OTHER INFORMATION:

RECEIVED

NOV 20

TECH CENTER

ENTERED

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49	ctgggagcct gcaagtgaac acagcctttg cggtccttag acagcttgcc ctggaggaga	180
51	acacatgaaa gaaagaacct caagaggctt tgttttctgt gaaacagtat ttctatacag	240
53	ttgctcca atg aca gag tta cct gca cgg ttg tcc tac ttc cag aat gca	290
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55	1 5 10	
57	cag atg tct gag gac aac cac ctg agc aat act gta cgt agc cag aat	338
58	Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	
59	15 20 25 30	
61	gac aat aga gaa cgg cag gag cac aac gac aga cgg agc ctt ggc cac	386
62	Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	
63	35 40 45	
65	cct gag cca tta tct aat gga cga ccc cag ggt aac tcc cgg cag gtg	434
66	Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val	
67	50 55 60	
69	gtg gag caa gat gag gaa gaa gat gag gag ctg aca ttg aaa tat ggc	482
70	Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	
71	65 70 75	
73	gcc aag cat gtg atc atg ctc ttt qtc cct gtg act ctc tgc atg gtg	530
74	Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val	
75	80 85 90	

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79 95      100      105      110
81 ggg cag cta atc tat acc cca ttc aca gaa gat acc gag act gtg ggc      626
82 Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly
83      115      120      125
85 cag aga gcc ctg cac tca att ctg aat gct gcc atc atg atc aqt gtc      674
86 Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val
87      130      135      140
89 att gtt gtc atg act atc ctc ctg gtg gtt ctg tat aaa tac agg tgc      722
90 Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys
91      145      150      155
93 tat aag gtc atc cat gcc tgg ctt att ata tca tct cta ttg ttg ctg      770
94 Tyr Lys Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu
95      160      165      170
97 ttc ttt ttt tca ttc att tac ttg ggg gaa gtg ttt aaa acc tat aac      818
98 Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn
99 175      180      185      190
101 gtt gct gtg gac tac att act gtt gca ctc ctg atc tgg aat ttt ggt      866
102 Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly
103      195      200      205
105 gtg gtg gga atg att tcc att cac tgg aaa ggt cca ctt cga ctc cag      914
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107      210      215      220
109 cag gca tat ctc att atg att agt gcc ctc atg gcc ctg gtg ttt atc      962
110 Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile
111      225      230      235
113 aag tac ctc cct gaa tgg act gcg tgg ctc atc ttg gct gtg att tca      1010
114 Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser
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123      275      280      285
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129 ccg gaa gct caa agg aga gta tcc aaa aat tcc aag cat aat gca gaa      1202
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133 agc aca gaa agg gag tca caa gac act gtt gca gag aat gat gat ggc      1250
134 Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly
135      320      325      330
137 ggg ttc agt gag gaa tgg gaa gcc cag agg gac agt cat cta ggg cct      1298
138 Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro
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141 cat cgc tct aca cct gaq tca cga gct gct gtc cag gaa ctt tcc agc      1346

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146 Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly
147          370          375          380
149 ttg gga gat ttc att ttc tac agt gtt ctg gtt ggt aaa gcc tca gca      1442
150 Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala
151          385          390          395
153 aca gcc agt gga gac tgg aac aca acc ata gcc tgt ttc gta gcc ata      1490
154 Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile
155          400          405          410
157 tta att ggt ttg tgc ctt aca tta tta ctc ctt gcc att ttc aag aaa      1538
158 Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys
159 415          420          425          430
161 gca ttg cca gct ctt cca atc tcc atc acc ttt ggg ctt gtt ttc tac      1586
162 Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr
163          435          440          445
165 ttt gcc aca gat tat ctt gta cag cct ttt atg gac caa tta gca ttc      1634
166 Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe
167          450          455          460
169 cat caa ttt tat atc tagcatatctt gcgggttagaa tcccatggat gttctctctt      1689
170 His Gln Phe Tyr Ile
171          465
173 tgactataac caaatctggg gaggacaaaag gtgattttcc tgtgtccaca tctaacaaag      1749
175 tcaagattcc cggetggact ttgcagctt ccttccaagt ctctctgacc accttgcact      1809
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179 actgtgtccc tcgggtgcaga aactaccaga tttagaggac gaggtcaagg agatatgata      1929
181 ggcgcggaag ttgctgtgcc ccatcagcag cttgacgcgt ggtcacagga cgatttcact      1989
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203 gcagctctgt crtggtagca gatgggtcca ttattctagg gtcttactct ttgtatgatg      2649
205 aaaagaatgt gttatgaatc ggtgctgtca gccctgctgt cagaccttct tccacagcaa      2709
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232	His	Val	Ile	Met	Leu	Phe	Val
233							
235	Val	Ala	Thr	Ile	Lys	Ser	Val
236							
238	Leu	Ile	Tyr	Thr	Pro	Phe	Thr
239							
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242							
244	Val	Met	Thr	Ile	Leu	Leu	Val
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247	Val	Ile	His	Ala	Trp	Leu	Ile
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250	Phe	Ser	Phe	Ile	Tyr	Leu	Gly
251							
253	Val	Asp	Tyr	Ile	Thr	Val	Ala
254							
256	Gly	Met	Ile	Ser	Ile	His	Trp
257							
259	Tyr	Leu	Ile	Met	Ile	Ser	Ala
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262	Leu	Pro	Glu	Trp	Thr	Ala	Trp
263							
265	Asp	Leu	Val	Ala	Val	Leu	Cys
266							
268	Glu	Thr	Ala	Gln	Glu	Arg	Asn
269							
271	Ser	Ser	Thr	Met	Val	Trp	Leu
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274	Ala	Gln	Arg	Arg	Val	Ser	Lys
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277	Glu	Arg	Glu	Ser	Gln	Asp	Thr
278							
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281							
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284							
286	Leu	Ala	Gly	Glu	Asp	Pro	Glu
287							
289	Asp	Phe	Ile	Phe	Tyr	Ser	Val
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292	Ser	Gly	Asp	Trp	Asn	Thr	Thr
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Input Set : A:\Sub_Seq_List_0609_4180002.txt

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 298 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
 299 435 440 445
 301 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
 302 450 455 460
 304 Phe Tyr Ile
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308 <210> SEQ ID NO: 3

309 <211> LENGTH: 2765

310 <212> TYPE: DNA

311 <213> ORGANISM: Homo sapiens

314 <220> FEATURE:

315 <221> NAME/KEY: CDS

316 <222> LOCATION: (249)..(1649)

317 <223> OTHER INFORMATION:

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 325 ctgggaacct gcaagtgcaca acagcctttg cggtccttag acagcttggc ctggaggaga 180
 327 acacatgaaa gaaagaacct caagaggctt tgttttctgt gaaacagtat ttctatacag 240
 329 ttgctcca atg aca gag tta cct gca ccg ttg tcc tac ttc cag aat gca 290
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 335 15 20 25 30
 337 gac aat aga gaa cgg cag gag cac aac gac aga cgg agc ctt ggc cac 386
 338 Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His
 339 35 40 45
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 342 Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val
 343 50 55 60
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 346 Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly
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 351 80 85 90
 353 gtg gtc gtg gct acc att aag tca gtc agc ttt tat acc cgg aag gat 578
 354 Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp
 355 95 100 105 110
 357 ggg cag cta atc tat acc cca ttc aca gaa gat acc gag act gtg ggc 626
 358 Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly
 359 115 120 125
 361 cag aga gcc ctg cac tca att ctg aat gct gcc atc atg atc agt gtc 674
 362 Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val
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RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\Sub_Seq_List_0609_4180002.txt
Output Set: N:\CRF4\11182002\I785474A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:25; Xaa Pos. 5